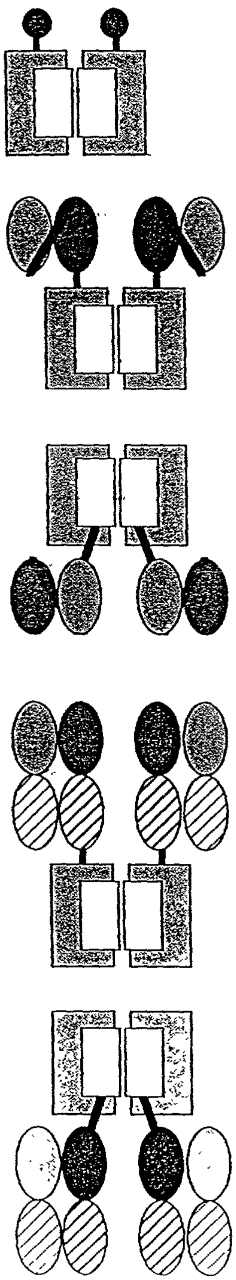
Figure 1



(A) Small ligand-Caspase Hetero-tetramer (after N-terminal processing)

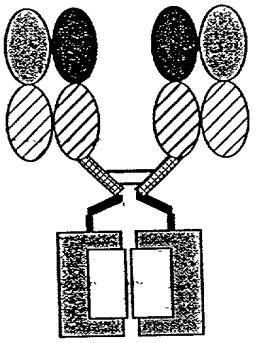
(B) Single-chain Fv (VL-VH format)-Caspase Hetero-tetramer

(C) Caspase Hetero-tetramer-Single-chain Fv (VL-VH format)

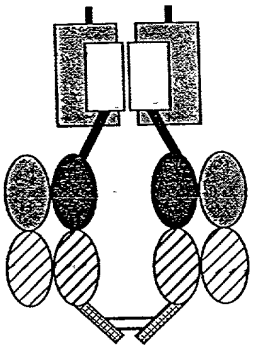
(D) Fab-(Heavy chain fusion) Caspase Hetero-tetramer

(E) Caspase Hetero-tetramer Fab-(Heavy chain fusion)

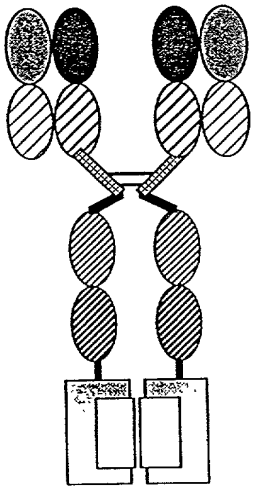
Figure 1 (cont)



(F) $F(ab')_2$-Caspase heterotetramer
Heavy chain fusion



(G) Caspase heterotetramer-F(ab')2
Heavy chain fusion



(H) IgG-Caspase heterotetramer

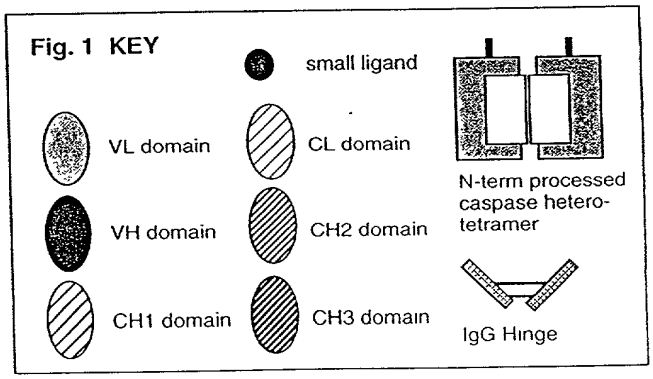


Figure 2

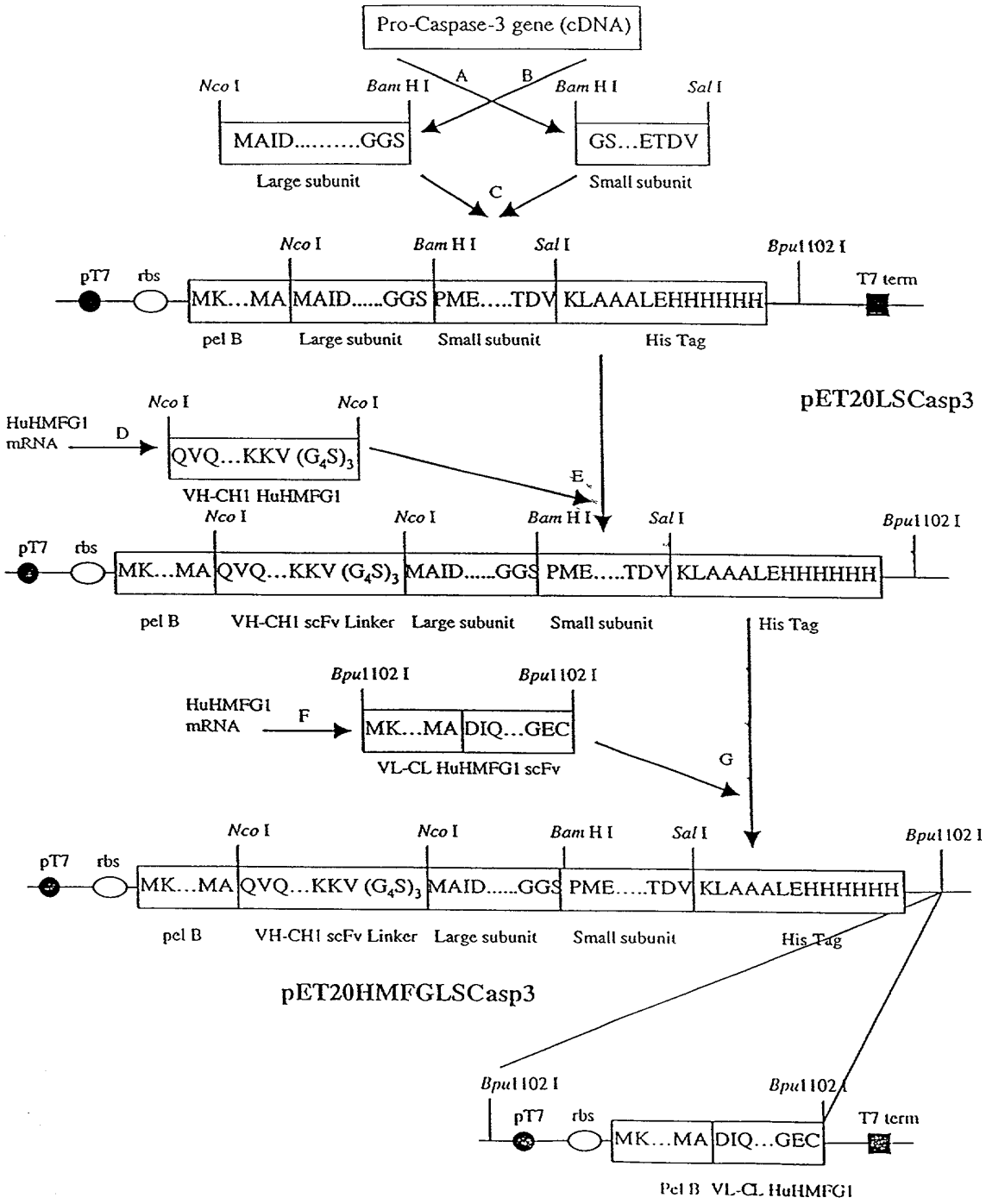

Pro-Caspase-3 gene (cDNA)
Nco I
Bam H I
A
B
Bam H I
Sal I
MAID.....GGS
GS...ETDV
Large subunit
Small subunit
C
Nco I
Bam H I
Sal I
Bpu1102 I
pT7
rbs
MK...MA
MAID.....GGS
PME.....TDV
KLAAALEHHHHHH
T7 term
pel B
Large subunit
Small subunit
His Tag
pET20LSCasp3
HuHMFG1
mRNA
D
Nco I
Nco I
QVQ...KKV (G4S)3
VH-CH1 HuHMFG1
E
Nco I
Nco I
Bam H I
Sal I
Bpu1102 I
pT7
rbs
MK...MA
QVQ...KKV (G4S)3
MAID.....GGS
PME.....TDV
KLAAALEHHHHHH
pel B
VH-CH1 scFv Linker
Large subunit
Small subunit
His Tag
Bpu1102 I
Bpu1102 I
HuHMFG1
mRNA
F
MK...MA
DIQ...GEC
VL-CL HuHMFG1 scFv
G
Nco I
Nco I
Bam H I
Sal I
Bpu1102 I
pT7
rbs
MK...MA
QVQ...KKV (G4S)3
MAID.....GGS
PME.....TDV
KLAAALEHHHHHH
pel B
VH-CH1 scFv Linker
Large subunit
Small subunit
His Tag
pET20HMFGLSCasp3
Bpu1102 I
Bpu1102 I
pT7
rbs
MK...MA
DIQ...GEC
T7 term
Pel B VL-CL HuHMFG1

Figure 3

```
1                                                                    60
ATGAAATACCTATTGCCTACGGCAGCCGCTGGATTGTTATTACTCGCGGCCCAGCCGGCC
 M  K  Y  L  L  P  T  A  A  A  G  L  L  L  L  A  A  Q  P  A

Nco I
61                                                                   120
ATGGCCCAGGTGCAGCTGGTGCAGTCTGGGGCAGAGGTGAAAAAGCCTGGGGCCTCAGTG
 M  A  Q  V  Q  L  V  Q  S  G  A  E  V  K  K  P  G  A  S  V

121                                                                  180
AAGGTGTCCTGCAAGGCTTCTGGCTACACCTTCAGTGCCTACTGGATAGAGTGGGTGCGC
 K  V  S  C  K  A  S  G  Y  T  F  S  A  Y  W  I  E  W  V  R

181                                                                  240
CAGGCTCCAGGAAAGGGCCTCGAGTGGGTCGGAGAGATTTTACCTGGAAGTAATAATTCT
 Q  A  P  G  K  G  L  E  W  V  G  E  I  L  P  G  S  N  N  S

241                                                                  300
AGATACAATGAGAAGTTCAAGGGCCGAGTGACAGTCACTAGAGACACATCCACAAACACA
 R  Y  N  E  K  F  K  G  R  V  T  V  T  R  D  T  S  T  N  T

301                                                                  360
GCCTACATGGAGCTCAGCAGCCTGAGGTCTGAGGACACAGCCGTCTATTACTGTGCAAGA
 A  Y  M  E  L  S  S  L  R  S  E  D  T  A  V  Y  Y  C  A  R

361                                                                  420
TCCTACGACTTTGCCTGGTTTGCTTACTGGGGCCAAGGGACTCTGGTCACAGTCTCCTCA
 S  Y  D  F  A  W  F  A  Y  W  G  Q  G  T  L  V  T  V  S  S
```

Figure 3 (cont)

421 480

GCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCTCCTCCAAGAGCACCTCTGGG

A S T K G P S V F P L A P S S K S T S G

481 540

GGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCG

G T A A L G C L V K D Y F P E P V T V S

541 600

TGGAACTCAGGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACAGTCCTCA

W N S G A L T S G V H T F P A V L Q S S

601 660

GGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACC

G L Y S L S S V V T V P S S S L G T Q T

661 720

TACATCTGCAACGTGAATCACAAGCCCAGCAACACCAAGGTGGACAAGAAAGTTGGTGGA

Y I C N V N H K P S N T K V D K K V G G

Nco I

721 780

GGCGGTTCAGGCGGAGGTGGCTCTGGTGGAGGCGGTTCCATGGCGATCGATACAGACAGT

G G S G G G G S G G G G S M A I D T D S

1261 1320

GGTGTTGATGATGACATGGCGTGTCATAAAATACCAGTGGATGCCGACTTCTTGTATGCA

G V D D D M A C H K I P V D A D F L Y A

1321 1380

TACTCCACAGCACCTGGTTATTATTCTTGGCGAAATTCAAAGGATGGCTCCTGGTTCATC

Y S T A P G Y Y S W R N S K D G S W F I

Figure 3 (cont)

```
1381                                                                1440
CAGTCGCTTTGTGCCATGCTGAAACAGTATGCCGACAAGCTTGAATTTATGCACATTCTT
 Q  S  L  C  A  M  L  K  Q  Y  A  D  K  L  E  F  M  H  I  L

1441                                                                1500
ACCCGGGTTAACCGAAAGGTGGCAACAGAATTTGAGTCCTTTTCCTTTGACGCTACTTTT
 T  R  V  N  R  K  V  A  T  E  F  E  S  F  S  F  D  A  T  F

1501                                                                1560
CATGCAAAGAAACAGATTCCATGTATTGTTTCCATGCTCACAAAAGAACTCTATTTTTAT
 H  A  K  K  Q  I  P  C  I  V  S  M  L  T  K  E  L  Y  F  Y

                    Bam HI
1561                                                                1620
CACGATGAAGTTGATGGTGGATCCCCGATGGAGAACACTGAAAACTACGTGGATTCAAAA
 H  D  E  V  D  G  G  S  P  M  E  N  T  E  N  S  V  D  S  K

781                                                                 840
TCCATTAAAAATTTGGAACCAAAGATCATACATGGAAGCGAATCAATGGACTCTGGAATA
 S  I  K  N  L  E  P  K  I  I  H  G  S  E  S  M  D  S  G  I

841                                                                 900
TCCCTGGACAACAGTTATAAAATGGATTATCCTGAGATGGGTTTATGTATAATAATTAAT
 S  L  D  N  S  Y  K  M  D  Y  P  E  M  G  L  C  I  I  I  N

901                                                                 960
AATAAGAATTTTCATAAAAGCACTGGAATGACATCTCGGTCTGGTACAGATGTCGATGCA
 N  K  N  F  H  K  S  T  G  M  T  S  R  S  G  T  D  V  D  A

961                                                                 1020
GCAAACCTCAGGGAAACATTCAGAAACTTGAAATATGAAGTCAGGAATAAAAATGATCTT
 A  N  L  R  E  T  F  R  N  L  K  Y  E  V  R  N  K  N  D  L
```

Figure 3 (cont)

1021 1080

ACACGTGAAGAAATTGTGGAATTGATGCGTGATGTTTCTAAAGAAGATCACAGCAAAAGG

T R E E I V E L M R D V S K E D H S K R

1081 1140

AGCAGTTTTGTTTGTGTGCTTCTGAGCCATGGTGAAGAAGGAATAATTTTTGGAACAAAT

S S F V C V L L S H G E E G I I F G T N

1141 1200

GGACCTGTTGACCTGAAAAAAATAACAAACTTTTTCAGAGGGGATCGTTGTAGAAGTCTA

G P V D L K K I T N F F R G D R C R S L

1201 1260

ACTGGAAAACCCAAACTTTTCATTATTCAGGCCTGCCGTGGTACAGAACTGGACTGTGGC

T G K P K L F I I Q A C R G T E L D C G

Sal I

1261 1320

ATTGAGACACAGGTCGACAAGCTTGCGGCCGCACTCGAGCACCACCACCACCACCACTGA

*I E T D V D K L A A A L E H H H H H H **

Bpu1102 I

1321 1380

GATCCGGCTGCTAACAAAGCCCGAAAGGGCTGAGTTGGCTGCTGCCACCGCTGAGCGAAA

1381 1440

TTAATACGACTCACTATAGGGAGACCACAACGGTTTCCCTCTAGAAATAATTTTGTTTAA

Figure 3 (cont)

```
1441                                                                1500
CTTTAAGAAGGAGATATACATATGAAATACCTATTGCCTACGGCAGCCGCTGGATTGTTA
                        M  K  Y  L  L  P  T  A  A  A  G  L  L

1501                                                                1560
TTACTCGCGGCCCAGCCGGCAATGGCCGACATCCAGATGACCCAGAGCCCAAGCAGCCTG
L  L  A  A  Q  P  A  M  A  D  I  Q  M  T  Q  S  P  S  S  L

1561                                                                1620
AGCGCCAGCGTGGGTGACAGAGTGACCATCACCTGTAAGTCCAGTCAGAGCCTTTTATAT
 S  A  S  V  G  D  R  V  T  I  T  C  K  S  S  Q  S  L  L  Y

1621                                                                1680
AGTAGCAATCAAAAGATCTACTTGGCCTGGTACCAGCAGAAGCCAGGTAAGGCTCCAAAG
 S  S  N  Q  K  I  Y  L  A  W  Y  Q  Q  K  P  G  K  A  P  K

1681                                                                1740
CTGCTGATCTACTGGGCATCCACTAGGGAATCTGGTGTGCCAAGCAGATTCAGCGGTAGC
 L  L  I  Y  W  A  S  T  R  E  S  G  V  P  S  R  F  S  G  S

1741                                                                1800
GGTAGCGGTACCGACTTCACCTTCACCATCAGCAGCCTCCAGCCAGAGGACATCGCCACC
 G  S  G  T  D  F  T  F  T  I  S  S  L  Q  P  E  D  I  A  T

1801                                                                1860
TACTACTGCCAGCAATATTATAGATATCCTCGGACGTTCGGCCAAGGGACCAAGGTGGAA
 Y  Y  C  Q  Q  Y  Y  R  Y  P  R  T  F  G  Q  G  T  K  V  E

1861                                                                1920
ATCAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTG
 I  K  R  T  V  A  A  P  S  V  F  I  F  P  P  S  D  E  Q  L
```

Figure 3 (cont)

1921 1980

AAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCCAAA

K S G T A S V V C L L N N F Y P R E A K

1981 2040

GTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTCACAGAG

V Q W K V D N A L Q S G N S Q E S V T E

2041 2100

CAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCCTGACGCTGAGCAAAGCAGAC

Q D S K D S T Y S L S S T L T L S K A D

2101 2160

TACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTC

Y E K H K V Y A C E V T H Q G L S S P V

Bpu1102 I

2161 2206

ACAAAGAGCTTCAACAGGGGAGAGTGTTAGTAGCAATGGGCTGAGC

*T K S F N R G E C * **

Figure 4

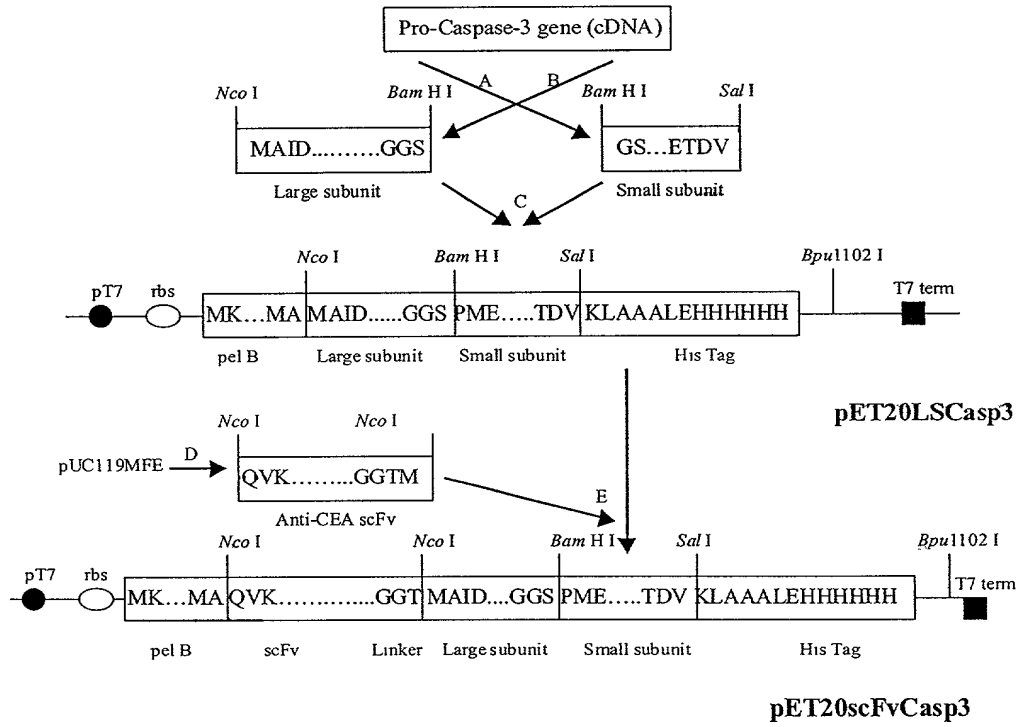

Pro-Caspase-3 gene (cDNA)
Nco I
Bam H I
A
B
Bam H I
Sal I
MAID.....GGS
GS...ETDV
Large subunit
Small subunit
C
Nco I
Bam H I
Sal I
Bpu1102 I
pT7
rbs
MK...MA
MAID.....GGS
PME.....TDV
KLAAALEHHHHHH
T7 term
pel B
Large subunit
Small subunit
His Tag
pET20LSCasp3
Nco I
Nco I
pUC119MFE
D
QVK.....GGTM
Anti-CEA scFv
E
Nco I
Nco I
Bam H I
Sal I
Bpu1102 I
pT7
rbs
MK...MA
QVK.....GGT
MAID....GGS
PME.....TDV
KLAAALEHHHHHH
T7 term
pel B
scFv
Linker
Large subunit
Small subunit
His Tag
pET20scFvCasp3

Figure 5

```
        10         20         30         40         50         60
CCATGGGGCAGGTGAAACTGCAGCAGTCTGGGGCAGAACTTGTGAGGTCAGGGACCTCAG
GGTACCCCGTCCACTTTGACGTCGTCAGACCCCGTCTTGAACACTCCAGTCCCTGGAGTC
   M  G  Q  V  K  L  Q  Q  S  G  A  E  L  V  R  S  G  T  S

        70         80         90        100        110        120
TCAAGTTGTCCTGCACAGCTTCTGGCTTCAACATTAAAGACTCCTATATGCACTGGTTGA
AGTTCAACAGGACGTGTCGAAGACCGAAGTTGTAATTTCTGAGGATATACGTGACCAACT
V  K  L  S  C  T  A  S  G  F  N  I  K  D  S  Y  M  H  W  L

       130        140        150        160        170        180
GGCAGGGGCCTGAACAGGGCCTGGAGTGGATTGGATGGATTGATCCTGAGAATGGTGATA
CCGTCCCCGGACTTGTCCCGGACCTCACCTAACCTACCTAACTAGGACTCTTACCACTAT
R  Q  G  P  E  Q  G  L  E  W  I  G  W  I  D  P  E  N  G  D

       190        200        210        220        230        240
CTGAATATGCCCCGAAGTTCCAGGGCAAGGCCACTTTTACTACAGACACATCCTCCAACA
GACTTATACGGGGCTTCAAGGTCCCGTTCCGGTGAAAATGATGTCTGTGTAGGAGGTTGT
T  E  Y  A  P  K  F  Q  G  K  A  T  F  T  T  D  T  S  S  N

       250        260        270        280        290        300
CAGCCTACCTGCAGCTCAGCAGCCTGACATCTGAGGACACTGCCGTCTATTATTGTAATG
GTCGGATGGACGTCGAGTCGTCGGACTGTAGACTCCTGTGACGGCAGATAATAACATTAC
T  A  Y  L  Q  L  S  S  L  T  S  E  D  T  A  V  Y  Y  C  N
```

Figure 5 (cont)

```
      310        320        330        340        350        360
AGGGGACTCCGACTGGGCCGTACTACTTTGACTACTGGGGCCAAGGGACCACGGTCACCG
TCCCCTGAGGCTGACCCGGCATGATGAAACTGATGACCCCGGTTCCCTGGTGCCAGTGGC
E  G  T  P  T  G  P  Y  Y  F  D  Y  W  G  Q  G  T  T  V  T

      370        380        390        400        410        420
TCTCCTCAGGTGGAGGCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGATCAGAAAATG
AGAGGAGTCCACCTCCGCCAAGTCCGCCTCCACCGAGACCGCCACCGCCTAGTCTTTTAC
V  S  S  G  G  G  G  S  G  G  G  G  S  G  G  G  G  S  E  N

      430        440        450        460        470        480
TGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAAGGTCACCATAACCT
ACGAGTGGGTCAGAGGTCGTTAGTACAGACGTAGAGGTCCCCTCTTCCAGTGGTATTGGA
V  L  T  Q  S  P  A  I  M  S  A  S  P  G  E  K  V  T  I  T

      490        500        510        520        530        540
GCAGTGCCAGCTCAAGTGTAAGTTACATGCACTGGTTCCAGCAGAAGCCAGGCACTTCTC
CGTCACGGTCGAGTTCACATTCAATGTACGTGACCAAGGTCGTCTTCGGTCCGTGAAGAG
C  S  A  S  S  S  V  S  Y  M  H  W  F  Q  Q  K  P  G  T  S

      550        560        570        580        590        600
CCAAACTCTGGATTTATAGCACATCCAACCTGGCTTCTGGAGTCCCTGCTCGCTTCAGTG
GGTTTGAGACCTAAATATCGTGTAGGTTGGACCGAAGACCTCAGGGACGAGCGAAGTCAC
P  K  L  W  I  Y  S  T  S  N  L  A  S  G  V  P  A  R  F  S
```

Figure 5 (cont)

```
610        620        630        640        650        660
GCAGTGGATCTGGGACCTCTTACTCTCTCACAATCAGCCGAATGGAGGCTGAAGATGCTG
CGTCACCTAGACCCTGGAGAATGAGAGAGTGTTAGTCGGCTTACCTCCGACTTCTACGAC
G  S  G  S  G  T  S  Y  S  L  T  I  S  R  M  E  A  E  D  A

670        680        690        700        710        720
CCACTTATTACTGCCAGCAAAGGAGTAGTTACCCACTCACGTTCGGTGCTGGCACCAAGC
GGTGAATAATGACGGTCGTTTCCTCATCAATGGGTGAGTGCAAGCCACGACCGTGGTTCG
A  T  Y  Y  C  Q  Q  R  S  S  Y  P  L  T  F  G  A  G  T  K

       730        740        750        760        770        780
TGGAGCTGCAACCGGGAGGTTCTGGAGGAACCATGGCGATCGATACAGACAGTGGTGTTG
ACCTCGACGTTGGCCCTCCAAGACCTCCTTGGTACCGCTAGCTATGTCTGTCACCACAAC
L  E  L  Q  P  G  G  S  G  G  T  M  A  I  D  T  D  S  G  V

       790        800        810        820        830        840
ATGATGACATGGCGTGTCATAAAATACCAGTGGATGCCGACTTCTTGTATGCATACTCCA
TACTACTGTACCGCACAGTATTTTATGGTCACCTACGGCTGAAGAACATACGTATGAGGT
D  D  D  M  A  C  H  K  I  P  V  D  A  D  F  L  Y  A  Y  S

       850        860        870        880        890        900
CAGCACCTGGTTATTATTCTTGGCGAAATTCAAAGGATGGCTCCTGGTTCATCCAGTCGC
GTCGTGGACCAATAATAAGAACCGCTTTAAGTTTCCTACCGAGGACCAAGTAGGTCAGCG
T  A  P  G  Y  Y  S  W  R  N  S  K  D  G  S  W  F  I  Q  S
```

Figure 5 (cont)

```
      910        920        930        940        950        960
TTTGTGCCATGCTGAAACAGTATGCCGACAAGCTTGAATTTATGCACATTCTTACCCGGG
AAACACGGTACGACTTTGTCATACGGCTGTTCGAACTTAAATACGTGTAAGAATGGGCCC
L  C  A  M  L  K  Q  Y  A  D  K  L  E  F  M  H  I  L  T  R

970        980        990       1000       1010       1020
TTAACCGAAAGGTGGCAACAGAATTTGAGTCCTTTTCCTTTGACGCTACTTTTCATGCAA
AATTGGCTTTCCACCGTTGTCTTAAACTCAGGAAAAGGAAACTGCGATGAAAAGTACGTT
V  N  R  K  V  A  T  E  F  E  S  F  S  F  D  A  T  F  H  A

      1030       1040       1050       1060       1070       1080
AGAAACAGATTCCATGTATTGTTTCCATGCTCACAAAAGAACTCTATTTTTATCACGATG
TCTTTGTCTAAGGTACATAACAAAGGTACGAGTGTTTTCTTGAGATAAAAATAGTGCTAC
K  K  Q  I  P  C  I  V  S  M  L  T  K  E  L  Y  F  Y  H  D

      1090       1100       1110       1120       1130       1140
AAGTTGATGGTGGATCCCCGATGGAGAACACTGAAAACTACGTGGATTCAAAATCCATTA
TTCAACTACCACCTAGGGGCTACCTCTTGTGACTTTTGATGCACCTAAGTTTTAGGTAAT
E  V  D  G  G  S  P  M  E  N  T  E  N  Y  V  D  S  K  S  I

      1150       1160       1170       1180       1190       1200
AAAATTTGGAACCAAAGATCATACATGGAAGCGAATCAATGGACTCTGGAATATCCCTGG
TTTTAAACCTTGGTTTCTAGTATGTACCTTCGCTTAGTTACCTGAGACCTTATAGGGACC
K  N  L  E  P  K  I  I  H  G  S  E  S  M  D  S  G  I  S  L
```

Figure 5 (cont)

```
      1210       1220       1230       1240       1250       1260
ACAACAGTTATAAAATGGATTATCCTGAGATGGGTTTATGTATAATAATTAATAATAAGA
TGTTGTCAATATTTTACCTAATAGGACTCTACCCAAATACATATTATTAATTATTATTCT
D  N  S  Y  K  M  D  Y  P  E  M  G  L  C  I  I  I  N  N  K

1270       1280       1290       1300       1310       1320
ATTTTCATAAAAGCACTGGAATGACATCTCGGTCTGGTACAGATGTCGATGCAGCAAACC
TAAAAGTATTTTCGTGACCTTACTGTAGAGCCAGACCATGTCTACAGCTACGTCGTTTGG
N  F  H  K  S  T  G  M  T  S  R  S  G  T  D  V  D  A  A  N

      1330       1340       1350       1360       1370       1380
TCAGGGAAACATTCAGAAACTTGAAATATGAAGTCAGGAATAAAAATGATCTTACACGTG
AGTCCCTTTGTAAGTCTTTGAACTTTATACTTCAGTCCTTATTTTTACTAGAATGTGCAC
L  R  E  T  F  R  N  L  K  Y  E  V  R  N  K  N  D  L  T  R

      1390       1400       1410       1420       1430       1440
AAGAAATTGTGGAATTGATGCGTGATGTTTCTAAAGAAGATCACAGCAAAAGGAGCAGTT
TTCTTTAACACCTTAACTACGCACTACAAAGATTTCTTCTAGTGTCGTTTTCCTCGTCAA
E  E  I  V  E  L  M  R  D  V  S  K  E  D  H  S  K  R  S  S

      1450       1460       1470       1480       1490       1500
TTGTTTGTGTGCTTCTGAGCCATGGTGAAGAAGGAATAATTTTTGGAACAAATGGACCTG
AACAAACACACGAAGACTCGGTACCACTTCTTCCTTATTAAAAACCTTGTTTACCTGGAC
F  V  C  V  L  L  S  H  G  E  E  G  I  I  F  G  T  N  G  P
```

Figure 5 (cont)

```
      1510       1520       1530       1540       1550       1560
TTGACCTGAAAAAAATAACAAACTTTTTCAGAGGGGATCGTTGTAGAAGTCTAACTGGAA
AACTGGACTTTTTTTATTGTTTGAAAAAGTCTCCCCTAGCAACATCTTCAGATTGACCTT
V  D  L  K  K  I  T  N  F  F  R  G  D  R  C  R  S  L  T  G

1570       1580       1590       1600       1610       1620
AACCCAAACTTTTCATTATTCAGGCCTGCCGTGGTACAGAACTGGACTGTGGCATTGAGA
TTGGGTTTGAAAAGTAATAAGTCCGGACGGCACCATGTCTTGACCTGACACCGTAACTCT
K  P  K  L  F  I  I  Q  A  C  R  G  T  E  L  D  C  G  I  E

      1630       1640       1650       1660       1670
CACAGGTCGACAAGCTTGCGGCCGCACTCGAGCACCACCACCACCACCACTGA
GTGTCCAGCTGTTCGAACGCCGGCGTGAGCTCGTGGTGGTGGTGGTGGTGACT
T  Q  V  D  K  L  A  A  A  L  E  H  H  H  H  H  H  *
```

Figure 6

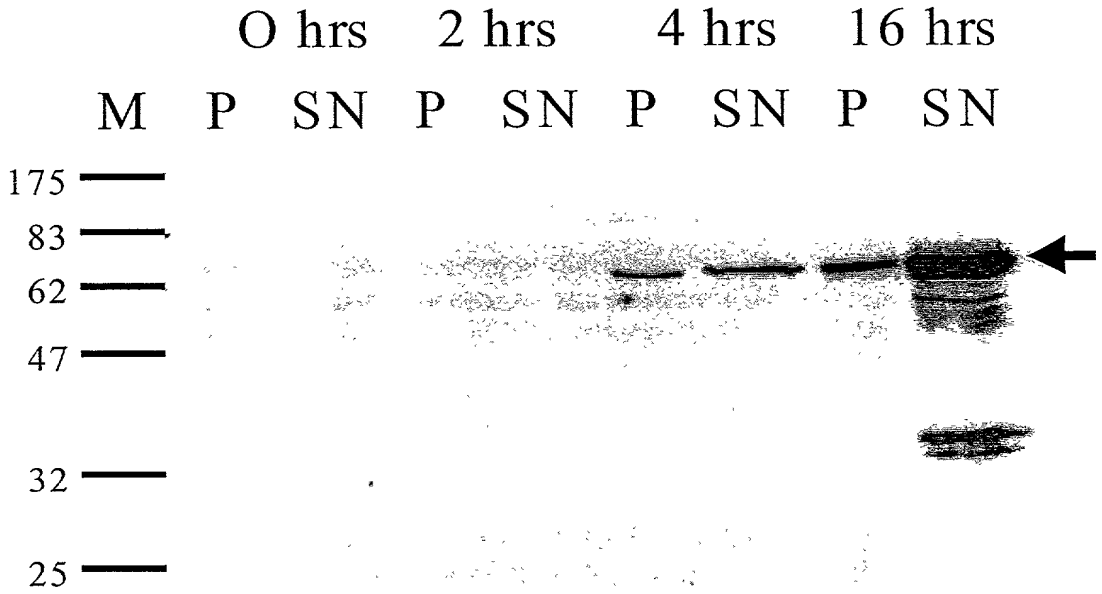


Figure 7

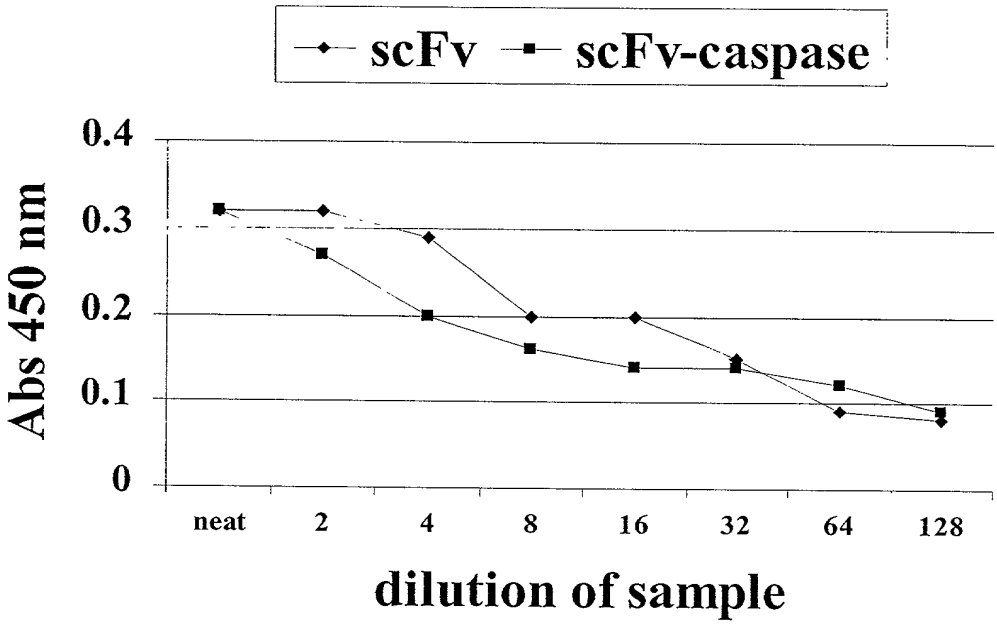

scFv
scFv-caspase
Abs 450 nm
0.4
0.3
0.2
0.1
0
neat
2
4
8
16
32
64
128
dilution of sample

Figure 8

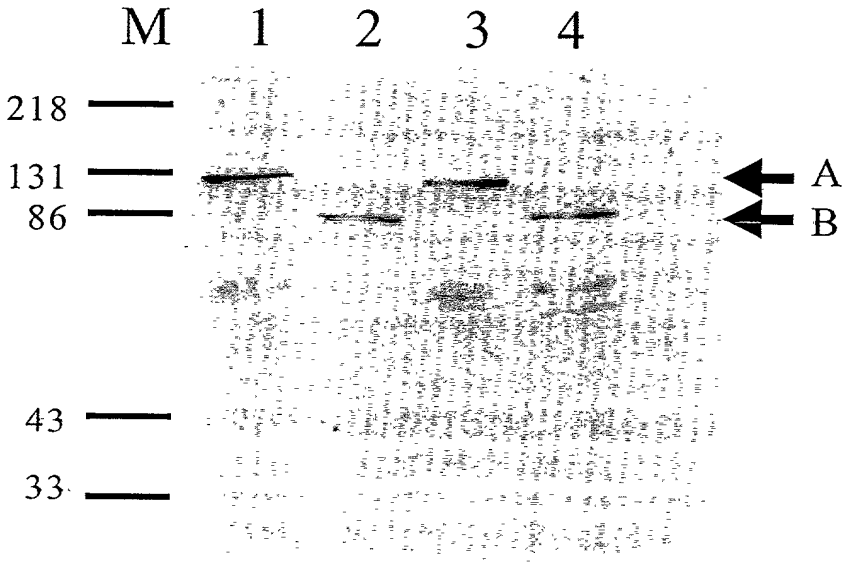
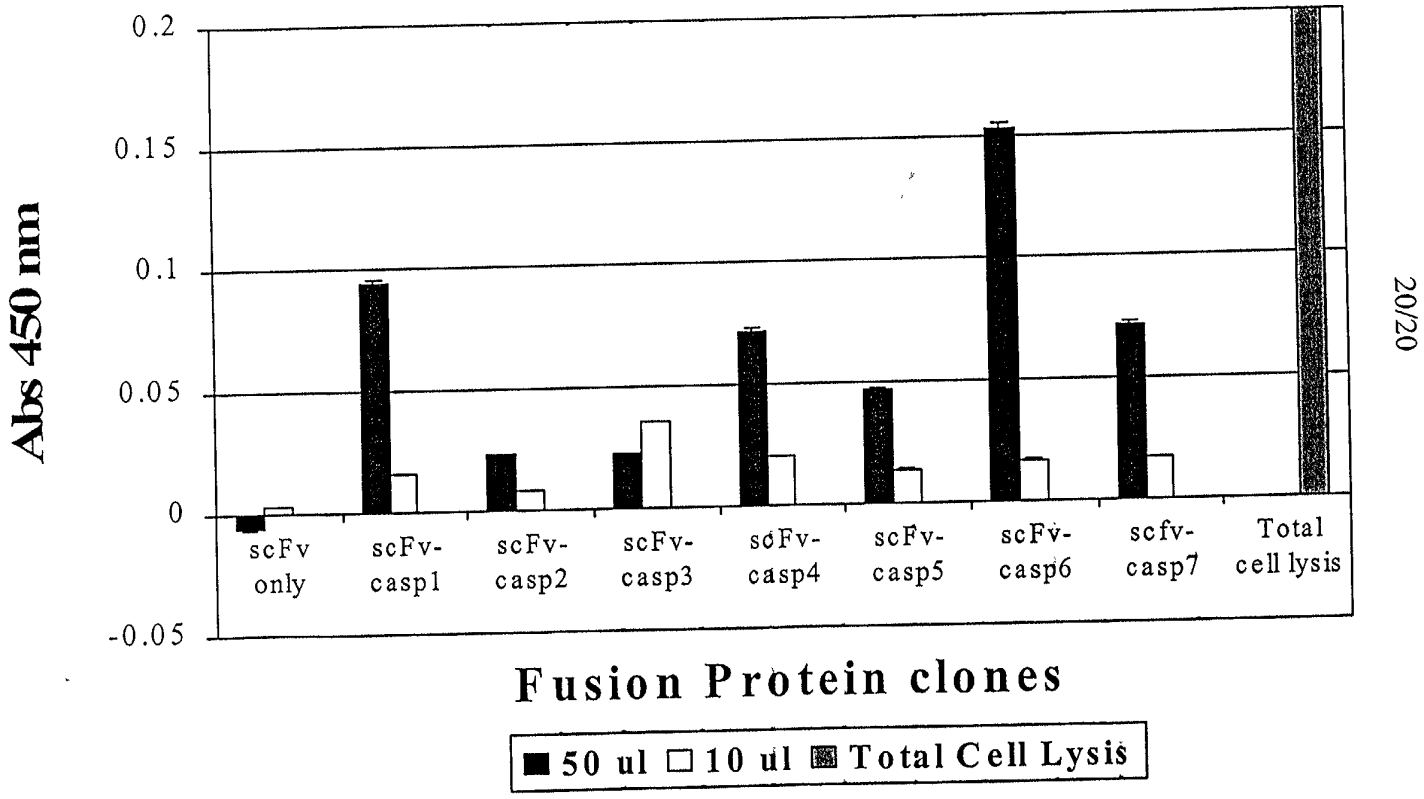


Figure 9


0.2
0.15
0.1
0.05
0
-0.05
Abs 450 nm
scFv only
scFv-casp1
scFv-casp2
scFv-casp3
scFv-casp4
scFv-casp5
scFv-casp6
scfv-casp7
Total cell lysis
Fusion Protein clones
50 ul
10 ul
Total Cell Lysis